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                   INPADOC
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E4           12     ALLENA M/AU
E5            7     ALLENA MARTA/AU
E6            2     ALLENACH D A/AU
E7            3     ALLENACH DAVID/AU
E8            2     ALLENAUSTIN D/AU
E9            1     ALLENB J/AU
E10           2     ALLENBACH/AU
E11           1     ALLENBACH A/AU
E12           1     ALLENBACH ALYCE/AU

=> e hitz, w/au
E1           15     HITZ WILLIAM DEAN/AU
E2            1     HITZ Y/AU
E3            0 --> HITZ, W/AU
E4            1     HITZAN R G/AU
E5            1     HITZANIDIS K/AU
E6            1     HITZANIDIS KYRIAKOS/AU
E7            2     HITZBLECH T/AU
E8            1     HITZBLECK E/AU
E9            1     HITZBLECK H/AU
E10           7     HITZBLECK J/AU
E11          16     HITZBLECK JULIA/AU
E12           1     HITZBLECK K/AU

=> s beta vulgaris
L1       14669 BETA VULGARIS

=> s l1 and (DNA encoding protein)
   5 FILES SEARCHED...
L2            0 L1 AND (DNA ENCODING PROTEIN)

=> s l1 and (sugar transplant protein)
L3            0 L1 AND (SUGAR TRANSPLANT PROTEIN)
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=> s (beta vulgaris sugar transport protein)
L4            5 (BETA VULGARIS SUGAR TRANSPORT PROTEIN)

=> d l4 ti abs ibib tot

L4   ANSWER 1 OF 5  WPIDS  COPYRIGHT 2006 THE THOMSON CORP on STN
TI   New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta
     vulgaris-like sugar transport protein, for altering the level of
     expression of a sugar transport protein in a host cell.
AN   2006-055117 [06]   WPIDS
CR   2002-453364 [48]; 2003-340957 [32]
AB   US2005282278 A UPAB: 20060124
     NOVELTY - An isolated nucleic acid fragment encoding all or a substantial
     portion of an Arabidopsis thaliana-like sugar transport protein, is new.
          DETAILED DESCRIPTION - A new isolated nucleic acid fragment encodes
     all or a substantial portion of an Arabidopsis thaliana-like sugar
     transport protein comprising a member selected from:
          (A) an isolated nucleic acid fragment encoding all or a substantial
     portion of the amino acid sequence set forth in a member selected from SEQ
     ID NO: 2, 4, 6, 8, 10, 12, 14 and 16, given in the specification;
          (B) an isolated nucleic acid fragment that is substantially similar
     to an isolated nucleic acid fragment encoding all or a substantial portion
     of the amino acid sequence set forth in a member selected from SEQ ID NO:
     2, 4, 6, 8, 10, 12, 14 and 16; and
          (C) an isolated nucleic acid fragment that is complementary to (a) or
     (b).
          INDEPENDENT CLAIMS are also included for:
          (1) an isolated nucleic acid fragment encoding all or a substantial
     portion of an Beta vulgaris-like sugar transport protein comprising a
     member selected from:
          (i) an isolated nucleic acid fragment encoding all or a substantial
     portion of the amino acid sequence set forth in a member selected from the
     group consisting of SEQ ID NO:18, 20, 22, 24, 26 and 28, given in the
     specification;
          (ii) an isolated nucleic acid fragment that is substantially similar
     to an isolated nucleic acid fragment encoding all or a substantial portion
     of the amino acid sequence set forth in a member selected from SEQ ID
     NO:18, 20, 22, 24, 26 and 28; and
          (iii) an isolated nucleic acid fragment that is complementary to or
     (b);
          (2) a chimeric gene comprising the nucleic acid fragment operably
     linked to suitable regulatory sequences;
          (3) a transformed host cell comprising the chimeric gene;
          (4) an Arabidopsis thaliana-like sugar transport protein polypeptide
     comprising all or a substantial portion of the amino acid sequence cited;
          (5) a Beta vulgaris sugar
     transport protein polypeptide comprising all or a
     substantial portion of the amino acid sequence cited;
          (6) a method of altering the level of expression of a sugar transport
     protein in a host cell;
          (7) a method of obtaining a nucleic acid fragment encoding all or a
     substantial portion of the amino acid sequence encoding a sugar transport
     protein; and
          (8) the product of the obtaining method.
          USE - The nucleic acid fragment is useful for altering the level of
     expression of a sugar transport protein in a host cell (claimed).
     Dwg.0/2
ACCESSION NUMBER:      2006-055117 [06]   WPIDS
CROSS REFERENCE:       2002-453364 [48]; 2003-340957 [32]
DOC. NO. CPI:          C2006-020697
TITLE:                 New nucleic acid fragment encoding a Arabidopsis
                       thaliana-like or Beta vulgaris-like sugar transport
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protein, for altering the level of expression of a sugar transport protein in a host cell.

DERWENT CLASS: C06 D16
INVENTOR(S): ALLEN, S M; HITZ, W D; KINNEY, A J; TINGEY, S V
PATENT ASSIGNEE(S): (ALLE-I) ALLEN S M; (HITZ-I) HITZ W D; (KINN-I) KINNEY A J; (TING-I) TINGEY S V
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2005282278	A1	20051222	(200606)*		59

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2005282278	A1 Div ex	US 2002-51902	20020117
		US 2005-210316	20050824

PRIORITY APPLN. INFO: US 2002-51902 20020117; US 2005-210316 20050824

L4 ANSWER 2 OF 5 WPIDS COPYRIGHT 2006 THE THOMSON CORP on STN
TI Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.
AN 2003-340957 [32] WPIDS
CR 2002-453364 [48]; 2006-055117 [06]
AB US2002178468 A UPAB: 20060124
NOVELTY - An Arabidopsis thaliana-like sugar transport protein (I) and a Beta vulgaris sugar transport protein (II), where (I) comprises eight fully defined sequences of, e.g. 747, 131, 131, and 737 amino acids in length and (II) comprises six fully defined sequences of, e.g. 167, 513, 510 and 523 amino acids in length, are new. Sequences given in the specification.

DETAILED DESCRIPTION - (I) comprises all or a substantial portion of the fully defined sequences of 747, 131, 131, 737, 486, 117, 345 and 228 amino acids in length and (II) comprises all or a substantial portion of the fully defined sequences of 167, 513, 510, 523, 539 and 529 amino acids in length.

INDEPENDENT CLAIMS are also included for:

(1) An isolated nucleic acid fragment (III)-(IV) comprising:
(a) A fragment encoding (I) or (II), respectively;
(b) A nucleic acid fragment that is similar to (III)-(IV), and
(c) An isolated nucleic acid fragment that is complementary to (III)-(IV);

(2) A chimeric gene (V) comprising (III) or (IV) operably linked to suitable regulatory sequences;

(3) A transformed host cell (VI) comprising (V);

(4) Obtaining (M1) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising:

(a) synthesizing an oligonucleotide primer corresponding to a portion of the nucleic acid sequence of (III) or (IV);

(b) amplifying a cDNA insert present in a cloning vector using the primers and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein;

(5) Obtaining (M2) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising:

(a) probing a cDNA or genomic library with (III) or (IV);
(b) identifying a DNA clone that hybridizes with (III) or (IV);
(c) isolating the DNA clone; and
(d) sequencing the cDNA or genomic fragment that comprise the clone; and
(6) The product of (M1) and (M2).
USE - The polypeptides may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with the chimeric construct (claimed). Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants.
Dwg.0/2

ACCESSION NUMBER: 2003-340957 [32] WPIDS
CROSS REFERENCE: 2002-453364 [48]; 2006-055117 [06]
DOC. NO. NON-CPI: N2003-272743
DOC. NO. CPI: C2003-089353
TITLE: Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein.
DERWENT CLASS: C06 D16 P13
INVENTOR(S): ALLEN, S M; HITZ, W D; KINNEY, A J; TINGEY, S V
PATENT ASSIGNEE(S): (ALLE-I) ALLEN S M; (HITZ-I) HITZ W D; (KINN-I) KINNEY A J; (TING-I) TINGEY S V
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002178468	A1	20021128	(200332)*		56

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
US 2002178468	A1 Provisional	US 1998-83044P	19980424
	Div ex	US 1999-291922	19990414
		US 2002-51902	20020117

FILING DETAILS:

PATENT NO	KIND	PATENT NO
US 2002178468	A1 Div ex	US 6383776

PRIORITY APPLN. INFO: US 1998-83044P 19980424; US 1999-291922 19990414; US 2002-51902 20020117

L4 ANSWER 3 OF 5 DGENE COPYRIGHT 2006 The Thomson Corp on STN
TI New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell.
AN AEE68545 protein DGENE
AB The invention comprise the amino acid and coding sequences of sugar transport proteins. The DNA and protein sequences of the invention are useful for altering the level of expression of a sugar transport protein in a host cell. The present amino acid sequence represents a sugar transport protein that was used in an example of the invention.
ACCESSION NUMBER: AEE68545 protein DGENE
TITLE: New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell.

INVENTOR: Allen S M; Hitz W D; Kinney A J; Tingey S V
PATENT ASSIGNEE: (ALLE-I)ALLEN S M.
(HITZ-I) HITZ W D.
(KINN-I) KINNEY A J.
(TING-I) TINGEY S V.
PATENT INFO: US 2005282278 A1 20051222 59
APPLICATION INFO: US 2005-210316 20050824
PRIORITY INFO: US 2002-51902 20020117
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2006-055117 [06]
DESCRIPTION: Beta vulgaris sugar transport protein amino acid sequence - SEQ ID 30.

L4 ANSWER 4 OF 5 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell;
plant recombinant protein isolation via transformed host cell for use in protein expression alteration
AN 2006-03652 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - An isolated nucleic acid fragment encoding all or a substantial portion of an Arabidopsis thaliana-like sugar transport protein, is new.
DETAILED DESCRIPTION - A new isolated nucleic acid fragment encodes all or a substantial portion of an Arabidopsis thaliana-like sugar transport protein comprising a member selected from: (A) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 and 16, given in the specification; (B) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 and 16; and (C) an isolated nucleic acid fragment that is complementary to (a) or (b). INDEPENDENT CLAIMS are also included for: (1) an isolated nucleic acid fragment encoding all or a substantial portion of an Beta vulgaris-like sugar transport protein comprising a member selected from: (i) an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:18, 20, 22, 24, 26 and 28, given in the specification; (ii) an isolated nucleic acid fragment that is substantially similar to an isolated nucleic acid fragment encoding all or a substantial portion of the amino acid sequence set forth in a member selected from SEQ ID NO:18, 20, 22, 24, 26 and 28; and (iii) an isolated nucleic acid fragment that is complementary to or (b); (2) a chimeric gene comprising the nucleic acid fragment operably linked to suitable regulatory sequences; (3) a transformed host cell comprising the chimeric gene; (4) an Arabidopsis thaliana-like sugar transport protein polypeptide comprising all or a substantial portion of the amino acid sequence cited; (5) a Beta vulgaris sugar transport protein polypeptide comprising all or a substantial portion of the amino acid sequence cited; (6) a method of altering the level of expression of a sugar transport protein in a host cell; (7) a method of obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a sugar transport protein; and (8) the product of the obtaining method.
BIOTECHNOLOGY - Preferred Method: Altering the level of expression of a sugar transport protein in a host cell comprises transforming a host cell with the chimeric gene, and growing the transformed host cell produced under conditions that are suitable for expression of the chimeric gene, where expression of the chimeric gene results in production of altered levels of a sugar transport protein in the

transformed host cell. Obtaining a nucleic acid fragment encoding all or a substantial portion of the amino acid sequence encoding a sugar transport protein comprises: (a) probing a cDNA or genomic library with the nucleic acid fragment;(b) identifying a DNA clone that hybridizes with the nucleic acid fragment; (c) isolating the DNA clone identified; and (d) sequencing the cDNA or genomic fragment that comprises the clone isolated, where the sequenced nucleic acid fragment encodes all or a substantial portion of the amino acid sequence encoding a sugar transport protein. The method alternatively comprises synthesizing an oligonucleotide primer corresponding to a portion of the sequence set forth in any of SEQ ID Nos. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25 and 27, and amplifying a cDNA insert present in a cloning vector using the oligonucleotide primer and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein.

USE - The nucleic acid fragment is useful for altering the level of expression of a sugar transport protein in a host cell (claimed).(59 pages)

ACCESSION NUMBER: 2006-03652 BIOTECHDS
TITLE: New nucleic acid fragment encoding a Arabidopsis thaliana-like or Beta vulgaris-like sugar transport protein, for altering the level of expression of a sugar transport protein in a host cell;
plant recombinant protein isolation via transformed host cell for use in protein expression alteration
AUTHOR: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V
PATENT ASSIGNEE: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V
PATENT INFO: US 2005282278 22 Dec 2005
APPLICATION INFO: US 2005-210316 24 Aug 2005
PRIORITY INFO: US 2005-210316 24 Aug 2005; US 2002-51902 17 Jan 2002
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2006-055117 [06]

L4 ANSWER 5 OF 5 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein;
involving vector plasmid-mediated gene transfer and expression in host cell for use in carbohydrate transport control
AN 2003-14205 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - An Arabidopsis thaliana-like sugar transport protein (I) and a Beta vulgaris sugar transport
protein (II), where (I) comprises eight fully defined sequences of, e.g. 747, 131, 131, and 737 amino acids in length and (II) comprises six fully defined sequences of, e.g. 167, 513, 510 and 523 amino acids in length, are new. Sequences given in the specification.

DETAILED DESCRIPTION - (I) comprises all or a substantial portion of the fully defined sequences of 747, 131, 131, 737, 486, 117, 345 and 228 amino acids in length and (II) comprises all or a substantial portion of the fully defined sequences of 167, 513, 510, 523, 539 and 529 amino acids in length. INDEPENDENT CLAIMS are also included for: (1) An isolated nucleic acid fragment (III)-(IV) comprising: (a) A fragment encoding (I) or (II), respectively; (b) A nucleic acid fragment that is similar to (III)-(IV), and (c) An isolated nucleic acid fragment that is complementary to (III)-(IV); (2) A chimeric gene (V) comprising (III) or (IV) operably linked to suitable regulatory sequences; (3) A transformed host cell (VI) comprising (V); (4) Obtaining (M1) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising: (a) synthesizing an oligonucleotide primer corresponding to a portion of the nucleic acid sequence of (III)

or (IV); (b) amplifying a cDNA insert present in a cloning vector using the primers and a primer representing sequences of the cloning vector, where the amplified nucleic acid fragment encodes a substantial portion of an amino acid sequence encoding a sugar transport protein; (5) Obtaining (M2) a nucleic acid fragment encoding a substantial portion of the amino acid sequence encoding a sugar transport protein comprising: (a) probing a cDNA or genomic library with (III) or (IV); (b) identifying a DNA clone that hybridizes with (III) or (IV); (c) isolating the DNA clone; and (d) sequencing the cDNA or genomic fragment that comprise the clone; and (6) The product of (M1) and (M2).

BIOTECHNOLOGY - Preparation: The proteins may be prepared according to standard recombinant methodologies.

USE - The polypeptides may be used for altering the level of expression of a sugar transport protein in a host cell, by transforming a host cell with the chimeric construct (claimed). Particularly, the polypeptides may provide a means to control carbohydrate transport and distribution in plants.

EXAMPLE - cDNA libraries representing mRNAs from various corn, rice, soybean and wheat tissues were prepared. The cDNAs were introduced into plasmid vectors by first preparing the cDNA libraries in Uni-ZAP XR vectors. The Uni-ZAP XR libraries were converted into plasmid libraries. The cDNAs were introduced directly into precut Bluescript vectors. Once the cDNA inserts were in plasmid vectors, the insert cDNA sequences were amplified by polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Insert DNAs were sequenced in dye-primer sequencing reactions to generate partial cDNA sequences. The resulting expressed sequence tags (ESTs) were analyzed using a sequencer. ESTs encoding sugar transport proteins were identified by conducting BLAST. The cDNA sequences were analyzed for similarity to all publicly available DNA sequences contained in the nr database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the nr database using the BLASTX algorithm provided by the NCBI. The BLASTX search using EST sequences from several corn, rice, soybean and wheat clones revealed similarity of the proteins encoded by the cDNAs to a sugar transport protein from Arabidopsis thaliana. In the process of comparing the ESTs it was found that many of the clones had overlapping regions of homology. Using this homology it was possible to align the ESTs and assemble and wheat sugar transport proteins. The sequence of the corn contig composed of clones p0032.crcba66r, p0097, cqran41r, crln.pk0143.h10, p0128, cpict38, p0106, cj1pm67r, cil1c.pk001.f21, p0072comgi92r, p0114, cimm181r and p0002.cgevb73r was 2824 nucleotides. The sequence of rice contig composed of clones r1r12.pk0013.d11 and rds1c.pk007.n17 was 443 nucleotides. The sequence of the entire cDNA inserts from clone r1s6.pk0003.d5 was 870 nucleotides fully defined in the specification. Similarly, Beta vulgaris sugar transport proteins were also identified and characterized. (56 pages)

ACCESSION NUMBER: 2003-14205 BIOTECHDS
TITLE: Novel plant sugar transport proteins and nucleic acid encoding the protein useful for producing transgenic plants having altered levels of sugar transport protein; involving vector plasmid-mediated gene transfer and expression in host cell for use in carbohydrate transport control
AUTHOR: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V
PATENT ASSIGNEE: ALLEN S M; HITZ W D; KINNEY A J; TINGEY S V
PATENT INFO: US 2002178468 28 Nov 2002
APPLICATION INFO: US 2002-51902 17 Jan 2002
PRIORITY INFO: US 2002-51902 17 Jan 2002; US 1998-83044 24 Apr 1998
DOCUMENT TYPE: Patent
LANGUAGE: English

OTHER SOURCE: WPI: 2003-340957 [32]

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FILE 'MEDLINE, BIOSIS, SCISEARCH, WPIDS, DGENE, EMBASE, BIOTECHDS, HCAPLUS' ENTERED AT 18:40:45 ON 29 AUG 2006
E ALLEN,S/AU
E HITZ, W/AU
L1 14669 S BETA VULGARIS
L2 0 S L1 AND (DNA ENCODING PROTEIN)
L3 0 S L1 AND (SUGAR TRANSPLANT PROTEIN)
L4 5 S (BETA VULGARIS SUGAR TRANSPORT PROTEIN)

=> s l1 and (DNA fragment)
L5 27 L1 AND (DNA FRAGMENT)

=> s l5 and (sugar transport protein)
L6 0 L5 AND (SUGAR TRANSPORT PROTEIN)

=> s l5 and (regulatory sequence0
UNMATCHED LEFT PARENTHESIS 'AND (REGULATORY'
The number of right parentheses in a query must be equal to the number of left parentheses.

=> s l5 and (regulatory sequence)
5 FILES SEARCHED...
L7 0 L5 AND (REGULATORY SEQUENCE)

=> s l5 and (protein)
L8 10 L5 AND (PROTEIN)

=> d l8 ti abs ibib tot

L8 ANSWER 1 OF 10 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
TI RECOMBINANT BEET CURLY TOP VIRUS GENOMES EXHIBIT BOTH PARENTAL AND NOVEL PATHOGENIC PHENOTYPES
AB Recombinant genomes derived from the Logan and CFH strains of the geminivirus beet curly top virus (BCTV) have been constructed and analyzed for pathogenicity on Nicotiana benthamiana and sugar beet (Beta vulgaris L.). Infectivity assays indicated that the latent period on N, benthamiana was primarily determined by a DNA fragment bearing the leftward open reading frames (ORFs) L1, L2, L3, and L4. Recombinants bearing leftward ORFs from the CFH strain were characterized as having a short latent period (mean = 6-11 days), while the reciprocal recombinants bearing leftward ORFs from the Logan strain had latent periods defined as long (mean = 16-22 days). Infectivity assays on sugar beet indicated that certain recombinant BCTV genomes exhibited novel pathogenic properties not common to either wild type strain, including the loss of systemic movement and replication competency, or asymptomatic systemic infection of sugar beet. The results indicate that N. benthamiana is a more permissive host than sugar beet with respect to heterologous combinations of BCTV genes, and that pathogenicity and virulence of BCTV in sugar beet requires the interaction of certain viral gene products and/or cis-elements that have coevolved in the same strain. (C) 1994 Academic Press, Inc.
ACCESSION NUMBER: 1994:244572 SCISEARCH
THE GENUINE ARTICLE: NG523
TITLE: RECOMBINANT BEET CURLY TOP VIRUS GENOMES EXHIBIT BOTH PARENTAL AND NOVEL PATHOGENIC PHENOTYPES

AUTHOR: STENGER D C (Reprint); DAVIS K R; BISARO D M
CORPORATE SOURCE: NO ILLINOIS UNIV, DEPT BIOL SCI, DE KALB, IL 60115 (Reprint); OHIO STATE UNIV, CTR BIOTECHNOL, COLUMBUS, OH 43210; OHIO STATE UNIV, DEPT PLANT BIOL, COLUMBUS, OH 43210; OHIO STATE UNIV, DEPT MOLEC GENET, COLUMBUS, OH 43210
COUNTRY OF AUTHOR: USA
SOURCE: VIROLOGY, (1 MAY 1994) Vol. 200, No. 2, pp. 677-685. ISSN: 0042-6822.
PUBLISHER: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 47
ENTRY DATE: Entered STN: 1994
Last Updated on STN: 1994
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L8 ANSWER 2 OF 10 DGENE COPYRIGHT 2006 The Thomson Corp on STN
TI Novel DNA used to produce transgenic plants with altered floral regulation which can have increased crop yields -
AN AAZ36962 DNA DGENE
AB The present sequence encodes a partial protein having a flowering regulating activity. Such protiens from Arabidopsis and rice are also disclosed, and are designated designated MPC1 and Os-MPC1, respectively. The rice and Arabidopsis cDNAs show significant homology with each other. A naturally occurring mutation of the MPC1 gene eliminates normal flowering regulating ability of plants, and leads to flowering immediately after germination (super early flowering mutation). The MPC1 polynucleotide sequence can be used to produce plants with altered flowering times in comparison with wild type plants, by enhancing or inhibiting the expression of the flowering regulating gene. Antisense polynucleotides can be used to reproduce the effects of the mutated MPC1 gene. This alteration can be used to increase the yield of food crops. Flowering inhibition of vegetables increases their productivity.
ACCESSION NUMBER: AAZ36962 DNA DGENE
TITLE: Novel DNA used to produce transgenic plants with altered floral regulation which can have increased crop yields -
INVENTOR: Yoshida N; Kato Y; Takahashi S; Yanai Y; Hiratsuka J; Miwa T
PATENT ASSIGNEE: (MITA)MITSUI CHEM INC.
PATENT INFO: EP 967278 A2 19991229 53
APPLICATION INFO: EP 1999-305077 19990628
PRIORITY INFO: JP 1998-180065 19980626
JP 1999-179043 19990624
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: 2000-064612 [06]
CROSS REFERENCES: P-PSDB: AAY53934
DESCRIPTION: DNA fragment encoding a flowering regulating protein.

L8 ANSWER 3 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Utilizing DNA containing all nucleotide sequences of spacer region of rDNA and whose G and C content exceeds 50% as enhancer which activates promoter of foreign cell;
new enhancer for use in transgenic plant construction
AN 2003-27031 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - Utilizing (M1) DNA (I) containing all the nucleotides sequences of spacer region of ribosomal DNA (rDNA), nucleotide sequence containing repeated rDNA spacer region sequence, or nucleotide sequence originating from the sequence and the total amount of G+C content exceeds 50%, as

enhancer which activates the promoter of a foreign cell.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following: (1) increasing (M2) expression in one or more foreign cell in one or more organ of plant by increasing activity of the promoter of one or more foreign gene involves use of (I); (2) chimeric gene (II) containing (I) and gene promoter, coding sequence or non-coding sequence and terminator sequence; (3) transformed plant (III) containing (II); and (4) cell in which expression of foreign gene is increased by (M1) and (M2).

BIOTECHNOLOGY - Preferred Method: In (M1), (I) hybridizes at 65degreesC in hybridization solution which consists of 3XSSC, 20 mM NaPO4 (pH 6.8) and is washed at 65degreesC in washing solution of 0.2X SSC, (I) hybridizes to DNA containing entire nucleotide sequences of spacer region of rDNA and nucleotide sequence comprising repeated rDNA spacer region, whose total amount of G+C content exceed 50%. Each of G and C is at least 25%, 30%, or 35%. (I) is derived from rice. (I) is isolated and/or purified DNA. In (M2), (I) is obtained from plant gene or produced artificially. Gene promoter is a promoter of plant. (I) increases the expression of green or non-green tissue of plant gene specifically in root, tuber, seed, stalk, flower or leaf of plant. The enhancer acts in both normal direction and reverse direction. A terminator is coupled with gene promoter. (III) is chosen from potato, tobacco, cotton, lettuce, melon, pumpkin, cucumber, pea, Brassica campestris (rapeseed plant), soybeans, sugar beet Helianthus annuus (sunflower), wheat, barley, rye wheat, rice, or maize.

USE - (I) is useful as an enhancer which activates the promoter of foreign cell. (M2) is useful for increasing gene expression in one or more foreign cell in one or more organ of a plant by increasing activity of a promoter of one or more foreign gene (claimed).

ADVANTAGE - The spacer region of rDNA with a high G+C content as enhancer increases the expression of foreign gene.

EXAMPLE - Expression of chimeric gene in transformed rice plant, which encode NADP type malic-acid enzyme was as follows. Ame1 cDNA which encoded NADP type malic-acid enzyme of aloe was isolated from pBluescript SK+ by digesting the vector with SmaI and KpnI. pLHC4 plasmid was digested by HindIII and SmaI, Cab promoter region was isolated. The DNA fragment of Cab promoter and cDNA of Ame1 were simultaneously cloned into pUC19. The obtained plasmid pUC19 was further cut by HindIII and SacI. The DNA fragment containing Cab promoter region and Ame1 cDNA were cloned to pBI-HI vector in which beta glucuronidase (GUS) gene was removed, where the hygromycin resistant gene is contained in pBI-HI. The obtained expression vector was named pBI-MC. The spacer region (3.2 kb) containing 25S rDNA(s) and a part of 17S rDNA(s) was obtained from pRR217 plasmid by digesting the plasmid with EcoRI and BamHI. The spacer region was cloned into pBluescript SK+. The obtained pBluescript SK+ was digested by XhoI and XbaI and 3.2 kb fragment obtained, was cloned into pUC19, and named pUC-SP. pUC-SP was digested by Sse83871 and XbaI and 3.2 kb fragment was obtained. The fragment was inserted into upstream of Cab promoter of pBI-MC. The expression vector was named pBI-MC/SP3.2. Agrobacterium tumefaciens was transformed with expression vector pBI-MC/SP3.2 and then was made to infect rice callus. Transformed rice callus was selected, after eliminating Agrobacterium, using hygromycin. A plant was regenerated from the selected resistant callus. In liquid nitrogen, leaves of transformed plant was fragmented, ground in 1.5 ml extraction buffer and centrifuged for 5 minutes at 15000 rpm at 4degreesC. The supernatant liquid was used as crude-enzyme liquid. To 50 mul of crude-enzyme liquid, 5 ml of sodium maleate aqueous solution was added and enzyme activity was computed from change of absorbence at 340 nm. The enzyme activity of six rice plants which had expression vector pBI-MC which did not contain the spacer area of rice rDNA and enzyme activity of eight rice plant which had expression vector pBI-MC/SP3.2 which contained the spacer region were compared. The results conformed that the spacer region was functioning as an enhancer

which increased expression of exogenous chimeric gene. (10 pages)
ACCESSION NUMBER: 2003-27031 BIOTECHDS
TITLE: Utilizing DNA containing all nucleotide sequences of spacer region of rDNA and whose G and C content exceeds 50% as enhancer which activates promoter of foreign cell; new enhancer for use in transgenic plant construction
PATENT ASSIGNEE: MITSUI CHEM INC
PATENT INFO: JP 2003135067 13 May 2003
APPLICATION INFO: JP 2001-332861 30 Oct 2001
PRIORITY INFO: JP 2001-332861 30 Oct 2001; JP 2001-332861 30 Oct 2001
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
OTHER SOURCE: WPI: 2003-771330 [73]

L8 ANSWER 4 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Novel herbicide resistant transformed sugar beet detectable by the specific primers to match the DNA sequences that flank the left and/or right border region of the inserted DNA; plasmid pMON17227-mediated Agrobacterium sp. phosphoshikimate-1-carboxyvinyltransferase gene transfer for herbicide resistance sugarbeet transgenic plant construction
AN 2002-19740 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - The transgenic glyphosate resistant sugar beet (I) comprising an insertion of DNA unique to T227-1 and its progeny detectable by either of the pair of primers for the left or right border, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) a pair of primers (II) comprising DNA which flank one of the border regions of the insertion of DNA into the T227-1 event; and (2) a polymerase chain reaction test using (II).

BIOTECHNOLOGY - Preferred Sugar Beet: (I) is detectable with the pair of primers identified as 98G94 and 98K86, 98150 and 98K89 or 98K89-RB12. (I) is detectable with the pair of primers that produce a fragment selected from 246 base pairs, 476 base pairs or 792 base pairs. (I) is characterized by an unique sequence of DNA having at least 80% homology to the right or left border sequence comprising genomic sugar beet DNA proximate the breakpoint of the insertion of the DNA into the genome and inserted plasmid DNA, where at least a 20 base pair fragment of the sequence of DNA is capable of detection by a pair of flanking primers where one of the primers is developed from the genomic sugar beet DNA proximate the breakpoint of the insertion of the DNA into the genome and one of the primers being developed from the inserted DNA plasmid. Preferred Primer: (II) comprises a DNA which lies in right border region of the insertion of DNA into the T227-1 event, where one primer lies in the plant genomic material and the other primer is in the inserted plasmid material. (II) comprises a DNA which lies in left border region of the insertion of DNA into the T227-1 event.

USE - (II) is useful in PCR (polymerase chain reaction) amplification to detect the presence or absence of the T227-1 event. (II) is also useful for detecting T227-1 event, by selecting sugar beet genomic material, employing the pair of primers capable of detecting the T227-1 event in association with such selected material, using a PCR machine to amplify the DNA fragment if it exists, and detecting the presence or the absence of the DNA fragment. (II) is also useful for detecting (I) characterized by T227-1 event with a test, by selecting sugar beet genomic material for testing, forming a pair of primers flanking the border sequence, where the primers are capable of detecting the glyphosate resistant sugar, using a PCR machine to amplify a unique DNA fragment produced through the use of the primers, if such fragment can be produced, and detecting the presence or absence of the DNA fragment (claimed).

EXAMPLE - The plasmid contained the left border, right border, the

FMV 35S promoter (from a modified figwort mosaic virus), and the main gene of interest to give glyphosate resistance the CP4 syn: the 5-enolpyruvylshikimate-3-phosphate synthase (CP4 EPSPS) gene from Agrobacterium sp. strain CP4. The plasmid also contained a chloroplast transit peptide and a terminator from pea. The circular vector pMON17227 opens at both left and right borders when inserted into the plant genome to form the transformed event. The selected transformation event was the T227-1 event. This transformed beet T227-1 and its progeny show excellent levels of glyphosphate tolerance. To characterize T227-1 fully, providing information that serves as a basis for event-specific polymerase chain reaction tests, the nucleotide sequences of the breakpoints between inserted vector and plant genomic DNA were determined. Genomic sequences flanking the T227-1 insert were isolated by linker PCR. Genomic DNA was digested and linkers attached to the ends of the fragments obtained. The fragments containing the T227-1 sequences were preferentially amplified using the linker sequence and pMON17227-specific sequences primers. The PCR products were sequenced, and the sequences used to design further primers, these were then used to amplify plant genomic DNA from the T227-1 transformant for both left and right borders (flanking sequences PCR) and from an untransformed plant. The first pair of primers was in the right border region of the inserted material. 98k89 was a primer that was located within the sugar beet plant genome. 98150 was a primer that was located in the inserted plasmid DNA sequence. In combination these primers, can be employed to produce a unique piece of DNA through a PCR test. This unique DNA specifically identifies this T227-1 transformation event. The sugar beet identified by this PCR flanking sequence was only the T227-1 event or its progeny. The second pair of primers was in the left border region of the inserted material. 98k86 was a primer that was located within the sugar beet plant genome. 98G94 was a primer that was located in the inserted plasmid DNA sequence. In combination these primers can be employed to produce a unique piece of DNA through a PCR test. These event specific tests using the primers include a method that employs electrophoresis through gels as the standard method used to separate, identify and purify DNA fragments. The location of the DNA that was separated by size within the gels can be determined by using a dye. This dye permits DNA bands with 1-10 ng of DNA to be detected under ultraviolet light. This unique DNA specifically identifies this T227-1 transformation event. The sugar beet identified by this PCR flanking sequence was only the T227-1 event or its progeny. Primers 98K89 and 98K86 for the T227-1 event or its progeny were situated in the regions flanking the inserted sequences, while 98150 and 98G94 lie inside the DNA from the vector. PCR with these primers was performed. In each 50 microl reaction, 50 ng of plant DNA was incubated with 120 ng of each primer and 1 U of Amplitaq DNA polymerase in GeneAmp PCR buffer II containing 10 mM Tris-HCl pH8.3 and 50 mM KCl complemented with 1.5 mM MgCl2 and 0.2 mM dNTP. 1 PCR reaction consisted of a hot start of 3 min. at 94degreesC followed by 35 cycles (one cycle: 30 seconds. at 94degreesC, 1 min, at 57degreesC and 1 min. at 72degreesC). The PCR products were separated on a 1.5% agarose gel. This amplification clearly demonstrated that the left and right flanking sequences were normally contiguous in sugar beet, and have not suffered major reorganization as a result of the transformation. (26 pages)

ACCESSION NUMBER: 2002-19740 BIOTECHDS

TITLE: Novel herbicide resistant transformed sugar beet detectable by the specific primers to match the DNA sequences that flank the left and/or right border region of the inserted DNA; plasmid pMON17227-mediated Agrobacterium sp. phosphoshikimate-1-carboxyvinyltransferase gene transfer for herbicide resistance sugarbeet transgenic plant construction

AUTHOR: WEYENS G; BARNES S; ROSQUE I

PATENT ASSIGNEE: SES EURO NV

PATENT INFO: WO 2002044407 6 Jun 2002

APPLICATION INFO: WO 2000-GB5321 30 Nov 2000
PRIORITY INFO: US 2000-250110 30 Nov 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-557546 [59]

L8 ANSWER 5 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence;
recombinant vector plasmid pBSK-mediated lipoxygenase gene transfer and expression in host cell and polymerase chain reaction for use as a fungicide, herbicide and pesticide
AN 2002-10155 BIOTECHDS
AB DERWENT ABSTRACT:
NOVELTY - An isolated nucleic acid molecule (a promoter of rice chemically induced cDNA (RCI-1) (I) capable of driving chemically-inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence, is new

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) an isolated nucleic acid molecule (II) which hybridizes under stringent conditions to a fully defined sequence of 358 (S1), 2104 (S2), 1516 (S3), 4569 (S17), 1198 (S18) or 2096 (S19) nucleotides as given in the specification, or to 4.5 kb PstI fragment (F) of plasmid pBSK+LOX4A which has been deposited under accession number DSM 13524, where the nucleic acid molecule drives chemically inducible but not wound- or pathogen-inducible expression of an operably-linked nucleotide sequence (2) an isolated nucleic acid molecule (III) which has a constitutive stretch of at least 50 nucleotides which has at least 70% sequence identity with a consecutive stretch of at least 50 nucleotides of (S1)-(S3), (S17)-(S19) or (F) as described above; (3) a recombinant nucleic acid molecule (IV) comprising (I), (II) or (III), operably linked to a nucleotide sequence of interest; (4) a nucleic acid expression vector (V) comprising (I)-(III) or (IV); (5) a host cell (VI) stably transformed with (I)-(III) or (IV); (6) a plant and its progeny (VII) stably transformed with (I)-(III) or (IV); (7) producing (I) by a polymerase chain reaction involves use of at least one oligonucleotide comprising a sequence of nucleotides which represents a consecutive stretch of 15 or more nucleotides of (S1)-(S3), (S17), or (S18) or (S19); (8) an isolated nucleic acid molecule (VIII) encoding a fully defined sequence of 37 amino acids (S6) as given in the specification, where the amino acid sequence (a transit peptide) is capable of targeting an associated protein to plastids; (9) a peptide (IX) encoded by (VIII); (10) an isolated nucleic acid molecule (X) which hybridizes under stringent conditions to a fully defined sequence of 3018 nucleotides (S5) as given in the specification and encodes a protein with lipoxygenase activity, where the protein encoded by the DNA has at least 65% amino acid sequence identity with the amino acid sequence of 922 amino acids (S7) fully defined in the specification; (11) a protein (XI) encoded by (X); (12) a recombinant nucleic acid molecule (XII) comprising (VIII) or (X); (13) a host cell stably transformed with (XII); (14) a plant or its progeny stably transformed with (XII); and (15) a seed of the above plant or its progeny.

BIOTECHNOLOGY - Preferred Nucleic Acid: . (I) is a component of the PstI/PstI fragment of about 4.5 kb in length from plasmid pBSK+LOX4A which has been deposited under Acc.Number DMS 13524. (I) is a component of the nucleotide sequence which has the fully defined sequence of (S17). (I) comprises (i) the nucleotide sequence of (S1), (ii) nucleotides 1-1358 of (S2), (iii) nucleotides 1702-2104 of (S2) and/or nucleotides 1-97 of (S3) and/or nucleotides 367-1283 of (S3), or (iv) a combination of any one of the nucleotide sequences of (S1)-(S3) or their portions. (III) comprises a stretch of 50 nucleotides having at least 70% sequence identity with a consecutive stretch of at least 50 nucleotides of

(S1)-(S3), (S17)-(S19) or to (F) as described above. (S1) is part of the 5' upstream sequence of rice chemically induced cDNA-1 (RCI-1) gene, (S2) is part of rice RCI-1 gene including putative TATA box and putative start codon, (S3) is part of the rice RCI-1 gene including part of intron 1, exon 2, intron 2 and part of exon 3, (S17) is nucleotide sequence of 4.5 kb PstI/PstI fragment from plasmid pBSK+lipoxygenase (LOX)4A, (S18) is a part of the 5' upstream sequence of the rice RCI-1 gene obtained by PCR, and (S19) is a part of the 5' upstream sequence of the rice RCI-1 gene obtained by PCR. (I), (II), and (III) are capable of driving the expression of an associated nucleotide sequence when induced by a chemical inducer such as BTH (benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester), INA (2,6-dichloroisonicotinic acid) or probenazole. Preferably, (I) drives expression of a nucleotide sequence when induced by jasmonic acid. (IV) comprises the isolated nucleic acid operably linked to a polypeptide coding sequence that comprises at its 5' end a nucleotide sequence encoding a fully defined lipoxygenase protein having the amino acid sequence of 37 amino acids as given in the specification. The coding sequence preferably encodes a desirable phenotypic trait. Optionally, the coding sequence is in antisense orientation. (X) preferably encodes a protein having a sequence of (S7). Preferred Host Cell: The host cell is a plant cell. Preferred Transformed Plant: The plant is a maize, wheat, sorghum, rye, oats, turf grass, rice, barley, soybean, cotton, tobacco, sugar beet or oilseed rape.

ACTIVITY - Plant antifungal. Details of test given but no results are stated.

MECHANISM OF ACTION - Fungal mycotoxin inhibitor. No data provided.

USE - (I), (II), (III) are useful for expressing a nucleotide sequence of interest. (IX) is useful for targeting an associated protein of interest to plastids. (X) which expresses polypeptide having lipoxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. (XI) is useful for inhibiting fungal mycotoxins (claimed). (I) is useful for regulating transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical regulator to a plant or seed containing a chemically regulatable nucleotide sequence. Transgenic plants as described above are useful for breeding improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to their optimized genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

EXAMPLE - Cloning of the rice chemically induced cDNA (RCI)-1 promoter region was carried out as follows. A lambda-DASH II/BamHI library representing genomic DNA derived from Oryza sativa cv. Norin plants was constructed. Screening of the library was carried out. The library was plated on four 530 cm2 bio-assay dishes. The plaques were transferred onto a nylon membrane. A 900 bp PstI-fragment representing the 5' end of the rice RCI-1 lipoxygenase cDNA clone pRC-1 having a fully defined sequence of 3018 nucleotides (S5) as given in the specification, was labeled with 32P and hybridized overnight at 65degreesC to plaque lifts. Two additional rounds of screening resulted in a positive lambda-clone (lambda lipoxygenase (LOX)4). The 4.5 kb DNA fragment was subcloned into a pBluescript/SK+vector and transformed into Escherichia coli strain DH5alpha cells and transformants were selected. This resulting clone was designated pBSK+LOX4A. Clone pBSK+LOX4A was deposited with the DSMZ with accession number DSM 13524. Clone pBSK+LOX4A contained the RCI-1 lipoxygenase promoter on a 4.5 kb PstI/PstI fragment and was further analyzed by DNA sequencing. Clone pBSK+LOX4A comprise, in a 5' to 3' direction, the nucleotide sequences (S1), (S2) and (S3). (S1) comprises the 5' end of the 4.5 kb PstI/PstI fragment. This nucleotide sequence was 358 nucleotides in length and

contained at its 5' end in position 1 to 6 the PstI-site. The region between (S1) and (S2) of the 4.5 kb PstI/PstI fragment was between about 240 and 440 bp in length. The central region of the 4.5 bp PstI/PstI fragment was (S2) and was 2104 bp in length. It contained the putative TATA box (position 1261 to 1266 (S2)), the putative start codon (position 1359 to 1361 of (S2)), as well as the 5' untranslated region and nucleotide sequences upstream of the putative TATA box. Comparison of the genomic DNA (S2) and the cDNA (S5) showed that the sequences located at position 1312 to 1701 of (S2) comprised all or part of exon 1, and the sequences located at position 1702 to 2104 of (S2) were the 5' part of intron 1. The region between (S2) and (S3) of the 4.5 kb PstI/PstI fragment was between about 85 and 285 bp in length. The 3' end of the 4.5 kb PstI/PstI fragment was (S3). This sequence depicted a nucleotide sequence of 1516 bp in length. It contained, in a 5' to 3' end of intron 1 (position 1 to 97 of (S3)) followed by exon 2 (position 98 to 366 of (S3)), intron 2 (position 367 to 1283 of (S3)) and part of exon 3 (position 1284 to 1516 of (S3)). The PstI site was located at position 1511 to 1516. (88 pages)

ACCESSION NUMBER: 2002-10155 BIOTECHDS
TITLE: Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence;
recombinant vector plasmid pBSK-mediated lipoxygenase gene transfer and expression in host cell and polymerase chain reaction for use as a fungicide, herbicide and pesticide
AUTHOR: DUDLER R; SCHAFFRATH; LAWTON K A
PATENT ASSIGNEE: SYNGENTA PARTICIPATIONS AG; UNIV ZUERICH
PATENT INFO: WO 2002006490 24 Jan 2002
APPLICATION INFO: WO 2000-EP8085 13 Jul 2000
PRIORITY INFO: GB 2000-22739 15 Sep 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-188550 [24]

L8 ANSWER 6 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to sugarbeet (Beta vulgaris) by introducing a DNA fragment having a nucleotide sequence which is homologous to the sequence of the genomic RNA-1 of BNYVV;
plasmid pVDH239 and plasmid pVDH240-mediated gene transfer and expression in transgenic plant
AN 2000-13300 BIOTECHDS
AB Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to a sugarbeet (Beta vulgaris) by introducing a DNA fragment of at least 15 bp in a sequence that is essentially homologous to the corresponding nucleotide sequence of the genomic RNA-1 of BNYVV. Also claimed are: a vector (plasmid pVDH239 and plasmid pVDH240) containing the DNA fragment; the use of the vector to transform plant cells using Agrobacterium tumefaciens; a plant cell containing the DNA fragment; the use of the plant cell for the regeneration of a sugarbeet that is resistant against BNYVV; a sugarbeet consisting at least partly of the plant cell; the progeny and seeds of the plant; and vegetatively reproducible structures such as calluses, buds and embryos derived from the sugar beet plant and seeds. The method is useful for conveying resistance to sugar beet plants against BNYVV and producing transgenic plants with complete immunity to BNYVV. Plant cells and other reproducible structures derived from these transgenic plants may be used for reproducing or regenerating subsequent generations of resistant sugar beet plants. (31pp)

ACCESSION NUMBER: 2000-13300 BIOTECHDS
TITLE: Conveying resistance to beet-necrotic-yellow-vein virus (BNYVV) to sugarbeet (Beta vulgaris) by

introducing a DNA fragment having a nucleotide sequence which is homologous to the sequence of the genomic RNA-1 of BNYVV; plasmid pVDH239 and plasmid pVDH240-mediated gene transfer and expression in transgenic plant

AUTHOR: Richards K; Jonard G; Guilley H; van dun C M P
PATENT ASSIGNEE: SES-Europe
LOCATION: Tiennen, Belgium.
PATENT INFO: WO 2000044915 3 Aug 2000
APPLICATION INFO: WO 2000-EP609 26 Jan 2000
PRIORITY INFO: EP 1999-200236 27 Jan 1999
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2000-505981 [45]

L8 ANSWER 7 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI DNA encoding scorpion peptide androctonin; vector-mediated gene transfer and expression in host cell or transgenic plant, used to confer disease-resistance
AN 1999-06262 BIOTECHDS
AB A new DNA fragment encodes androctonin (AD). Also new are: a DNA fragment encoding a peptide-AD or AD-peptide fusion protein; a fusion protein encoded by the DNA; a chimeric gene consisting of the new DNA linked to expression regulatory sequences; a cloning or expression vector containing the chimeric DNA; a host cell (preferably a plant cell) transformed with the vector; plants containing the transformed cells; and seeds of the transgenic plant. The DNA can be used to produce transgenic plants with disease-resistance against bacterial or fungal infections, especially infection caused by Cercospora beticola, Cladosporium herbarum, Fusarium cuulmorum, Fusarium graminearum or Phytophthora cinnamomi. The host cell may be a bacterium such as Escherichia coli, a yeast such as Saccharomyces sp., Kluyveromyces sp. or Pichia sp., a fungus such as Aspergillus sp., a baculo virus or a plant cell. The transgenic plant may be maize (Zea mays), wheat (Triticum aestivum), rape (Brassica napus), soybean (Glycine max), rice (Oryza sativa), sugarcane (Saccharum officinale), sugarbeet (Beta vulgaris), tobacco (Nicotiana tabacum) or cotton (Gossypium hirsutum). (37pp)
ACCESSION NUMBER: 1999-06262 BIOTECHDS
TITLE: DNA encoding scorpion peptide androctonin; vector-mediated gene transfer and expression in host cell or transgenic plant, used to confer disease-resistance
AUTHOR: Freyssinet G; Derose R; Hoffmann J
PATENT ASSIGNEE: Rhone-Poulenc-Agrochem.
LOCATION: Lyons, France.
PATENT INFO: WO 9909189 25 Feb 1999
APPLICATION INFO: WO 1998-FR1814 18 Aug 1998
PRIORITY INFO: FR 1997-10632 20 Aug 1997
DOCUMENT TYPE: Patent
LANGUAGE: French
OTHER SOURCE: WPI: 1999-181046 [15]

L8 ANSWER 8 OF 10 BIOTECHDS COPYRIGHT 2006 THE THOMSON CORP. on STN
TI DNA fragment encoding alpha-amylase in dicotyledonous plant; fusion protein gene cloning and controlled expression in Escherichia coli, Bacillus subtilis, Aspergillus sp., Agrobacterium sp. or potato; DNA probe construction; DNA sequence
AN 1991-02153 BIOTECHDS
AB The following are claimed: an AmyZ4 or AmyZ6 gene (A) from a dicotyledonous plant, encoding an alpha-amylase (EC-3.2.1.1), and with regulatory regions, a promoter, a coding region, introns and transcription terminators, possibly labeled; DNA encoding a fusion

protein, with (A) and at least 1 other polypeptide gene; a purified polypeptide, encoded by (A) and free of other naturally occurring enzymes; DNA encoding an antisense RNA complementary to (A) mRNA and inhibiting its translation; antisense DNA for (A) under the control of a promoter for production of antisense RNA; single-stranded DNA or RNA complementary to either strand of (A); a vector carrying any of these fragments; a host, e.g. Bacillus subtilis, Saccharomyces cerevisiae, Aspergillus sp., Agrobacterium sp. or (preferably) Escherichia coli K12 (DSM 5275, DSM 5276, DSM 5882, DSM 5883, or DSM 5884) or a transgenic plant, preferably potato (Solanum tuberosum), containing (A); and methods for production of these. (A) is used for controlled expression of alpha-amylase activity, and is useful as a DNA probe for quantification of (A) mRNA for use e.g. in the food and alcohol industries. (155pp)

ACCESSION NUMBER: 1991-02153 BIOTECHDS
TITLE: DNA fragment encoding alpha-amylase in dicotyledonous plant; fusion protein gene cloning and controlled expression in Escherichia coli, Bacillus subtilis, Aspergillus sp., Agrobacterium sp. or potato; DNA probe construction; DNA sequence
PATENT ASSIGNEE: Danisco
PATENT INFO: WO 9012876 1 Nov 1990
APPLICATION INFO: WO 1990-DK108 24 Apr 1990
PRIORITY INFO: DK 1989-1980 24 Apr 1989
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1990-348479 [46]

L8 ANSWER 9 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
TI Elimination of transcriptional interference between tandem genes in plant cells
AB This invention relates to the field of biotechnol. or genetic engineering. Specifically, this invention relates to the field of gene expression. More specifically, this invention relates to methods to reduce or eliminate transcriptional interference between two or more tandemly arranged genes within a host cell.

ACCESSION NUMBER: 2002:814750 HCAPLUS
DOCUMENT NUMBER: 137:334040
TITLE: Elimination of transcriptional interference between tandem genes in plant cells
INVENTOR(S): Padidam, Malla
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 33 pp. CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2002155540	A1	20021024	US 2002-74744		20020213
PRIORITY APPLN. INFO.:			US 2001-268584P	P	20010214

L8 ANSWER 10 OF 10 HCAPLUS COPYRIGHT 2006 ACS on STN
TI PCR-based cloning and segregation analysis of functional gene homologues in Beta vulgaris
AB To analyze genetic factors that potentially affect sugar quality and yield in Beta vulgaris, we designed primers based on 18 homologous ESTs and conserved regions of 32 heterologous ESTs encoding gene products that act in the Calvin cycle, the oxidative pentose phosphate cycle, photorespiration, synthesis, transport and degradation of

sucrose, glycolysis, the citric acid cycle, nitrogen metabolism and osmoprotection. Data on the amplification of 54 gene homologues from B. vulgaris are presented. Among these are 35 homologues for which DNA sequence information from B. vulgaris is now available for the first time. For genetic mapping a PCR-based strategy using CAPS (cleaved amplified polymorphic sequence), DFLP (DNA fragment length polymorphism), SSCP (single-strand conformation polymorphism) and HD (heteroduplex) anal. was adopted. RFLP anal. was also used in some cases. The different techniques used for the detection of polymorphisms are evaluated with respect to their sensitivity and versatility. In all, 42 functional genes have been assigned to the nine linkage groups of sugar beet.

ACCESSION NUMBER: 1999:796844 HCAPLUS
DOCUMENT NUMBER: 132:147436

TITLE: PCR-based cloning and segregation analysis of functional gene homologues in Beta vulgaris

AUTHOR(S): Schneider, K.; Borchardt, D. C.; Schafer-Pregl, R.; Nagl, N.; Glass, C.; Jeppsson, A.; Gebhardt, C.; Salamini, F.
CORPORATE SOURCE: Max-Planck-Institut fur Zuchtungsforschung, Koln, D-50829, Germany

SOURCE: Molecular and General Genetics (1999), 262(3), 515-524
CODEN: MGGEAE; ISSN: 0026-8925
PUBLISHER: Springer-Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

Refine Search

Search Results -

Terms	Documents
L8 and L5	866

Database:
- US Pre-Grant Publication Full-Text Database
- US Patents Full-Text Database
- US OCR Full-Text Database
- EPO Abstracts Database
- JPO Abstracts Database
- Derwent World Patents Index
- IBM Technical Disclosure Bulletins

Search: L9

Refine Search | Recall Text | Clear | Interrupt

Search History

DATE: Tuesday, August 29, 2006 Purge Queries | Printable Copy | Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=PGPB; PLUR=YES; OP=OR			
L9	L8 and l5	866	L9
L8	allen.in.	6781	L8
DB=USPT; PLUR=YES; OP=OR			
L7	L5 and (sugar transport protein)	0	L7
L6	L5 and (DNA encoding protein)	0	L6
DB=PGPB; PLUR=YES; OP=OR			
L5	beta vulgaris	138458	L5
L4	L1 and (beta vulgaris)	1	L4
L3	L1 and (90%)	1	L3
L2	L1 and (isolated cell)	1	L2
L1	20020178468	1	L1

END OF SEARCH HISTORY

Refine Search

Search Results -

Terms	Documents
6383776.pn.	1

Database:
- US Pre-Grant Publication Full-Text Database
- **US Patents Full-Text Database**
- US OCR Full-Text Database
- EPO Abstracts Database
- JPO Abstracts Database
- Derwent World Patents Index
- IBM Technical Disclosure Bulletins

Search: L18

Refine Search | Recall Text | Clear | Interrupt

Search History

DATE: Tuesday, August 29, 2006 **Purge Queries** Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT; PLUR=YES; OP=OR			
L18	6383776.pn.	1	L18
L17	7041476.pn.	1	L17
DB=USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L16	L15	0	L16
DB=PGPB; PLUR=YES; OP=OR			
L15	L14 and (DNA complement)	346	L15
L14	L13 and (transform cell)	366	L14
L13	L12 and (regulatory sequence)	366	L13
L12	L11 and (fragment)	371	L12
L11	L10 and (DNA encoding protein)	561	L11
L10	L9 and (sugar transport protein)	651	L10
L9	L8 and l5	866	L9
L8	allen.in.	6781	L8
DB=USPT; PLUR=YES; OP=OR			
L7	L5 and (sugar transport protein)	0	L7
L6	L5 and (DNA encoding protein)	0	L6
DB=PGPB; PLUR=YES; OP=OR			
L5	beta vulgaris	138458	L5
L4	L1 and (beta vulgaris)	1	L4

L3	L1 and (90%)	1	L3
L2	L1 and (isolated cell)	1	L2
L1	20020178468	1	L1

END OF SEARCH HISTORY